



SEQUENCE LISTING

<110> Kabushiki Kaisha Hayashibara Seibutsu Kagaku Kenkyujo
ARIYASU, Toshio
MATSUMOTO, Shuji
KYONO, Fumiyo
HANAYA, Toshiharu
ARAI, Shigeyuki
IKEDA, Masao
KURIMOTO, Masashi

<120> TREHALOSE RECEPTOR AND METHOD FOR DETECTING TREHALOSE WITH THE SAME

<130> ARIYASU2

<140> 10/663,650
<141> 2003-09-17

<160> 24

<170> PatentIn version 3.3

<210> 1
<211> 374
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> GENBANK Accession no. M80632

<400> 1

Met Ala Arg Ser Leu Thr Trp Gly Cys Cys Pro Trp Cys Leu Thr Glu
1 5 10 15

Glu Glu Lys Thr Ala Ala Arg Ile Asp Gln Glu Ile Asn Arg Ile Leu
20 25 30

Leu Glu Gln Lys Lys Gln Glu Arg Glu Glu Leu Lys Leu Leu Leu
35 40 45

Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
50 55 60

Ile His Gly Val Gly Tyr Ser Glu Glu Asp Arg Arg Ala Phe Arg Leu
65 70 75 80

Leu Ile Tyr Gln Asn Ile Phe Val Ser Met Gln Ala Met Ile Asp Ala
85 90 95

Met Asp Arg Leu Gln Ile Pro Phe Ser Arg Pro Asp Ser Lys Gln His
100 105 110

Ala Ser Leu Val Met Thr Gln Asp Pro Tyr Lys Val Ser Thr Phe Glu
115 120 125

Lys Pro Tyr Ala Val Ala Met Gln Tyr Leu Trp Arg Asp Ala Gly Ile
130 135 140

Arg Ala Cys Tyr Glu Arg Arg Glu Phe His Leu Leu Asp Ser Ala
145 150 155 160

Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Ser Glu Asp Ser Tyr Ile
165 170 175

Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
180 185 190

Asn Glu Tyr Cys Phe Ser Val Lys Lys Thr Lys Leu Arg Ile Val Asp
195 200 205

Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu
210 215 220

Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
225 230 235 240

Cys Leu Glu Glu Asn Asp Gln Glu Asn Arg Met Glu Glu Ser Leu Ala
245 250 255

Leu Phe Ser Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
260 265 270

Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Asp Lys Ile His Thr
275 280 285

Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Arg Arg Asp
290 295 300

Ala Glu Ala Ala Lys Ser Phe Ile Leu Asp Met Tyr Ala Arg Val Tyr
305 310 315 320

Ala Ser Cys Ala Glu Pro Gln Asp Gly Gly Arg Lys Gly Ser Arg Ala

325

330

335

Arg Arg Phe Phe Ala His Phe Thr Cys Ala Thr Asp Thr Gln Ser Val
340 345 350

Arg Ser Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu
355 360 365

Asp Glu Ile Asn Leu Leu
370

<210> 2
<211> 374
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> GENBANK Accession no. M63904

<400> 2

Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu
1 5 10 15

Asp Glu Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu
20 25 30

Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu
35 40 45

Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
50 55 60

Ile His Gly Ala Gly Tyr Ser Glu Glu Arg Lys Gly Phe Arg Pro
65 70 75 80

Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala
85 90 95

Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His
100 105 110

Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu
115 120 125

Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile
130 135 140

Arg Ala Cys Tyr Glu Arg Arg Glu Phe His Leu Leu Asp Ser Ala
145 150 155 160

Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val
165 170 175

Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
180 185 190

Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp
195 200 205

Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu
210 215 220

Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
225 230 235 240

Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala
245 250 255

Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
260 265 270

Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr
275 280 285

Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp
290 295 300

Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr
305 310 315 320

Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Lys Lys Gly Ala Arg Ser
325 330 335

Arg Arg Leu Phe Ser His Tyr Thr Cys Ala Thr Asp Thr Gln Asn Ile
340 345 350

Arg Lys Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu

355

360

365

Asp Glu Ile Asn Leu Leu
370

<210> 3
<211> 355
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> GENBANK Accession no. NM_002073

<400> 3

Met Gly Cys Arg Gln Ser Ser Glu Glu Lys Glu Ala Ala Arg Arg Ser
1 5 10 15

Arg Arg Ile Asp Arg His Leu Arg Ser Glu Ser Gln Arg Gln Arg Arg
20 25 30

Glu Ile Lys Leu Leu Leu Gly Thr Ser Asn Ser Gly Lys Ser Thr
35 40 45

Ile Val Lys Gln Met Lys Ile Ile His Ser Gly Gly Phe Asn Leu Glu
50 55 60

Ala Cys Lys Glu Tyr Lys Pro Leu Ile Ile Tyr Asn Ala Ile Asp Ser
65 70 75 80

Leu Thr Arg Ile Ile Arg Ala Leu Ala Ala Leu Arg Ile Asp Phe His
85 90 95

Asn Pro Asp Arg Ala Tyr Asp Ala Val Gln Leu Phe Ala Leu Thr Gly
100 105 110

Pro Ala Glu Ser Lys Gly Glu Ile Thr Pro Glu Leu Leu Gly Val Met
115 120 125

Arg Arg Leu Trp Ala Asp Pro Gly Ala Gln Ala Cys Phe Ser Arg Ser
130 135 140

Ser Glu Tyr His Leu Glu Asp Asn Ala Ala Tyr Tyr Leu Asn Asp Leu
145 150 155 160

Glu Arg Ile Ala Ala Ala Asp Tyr Ile Pro Thr Val Glu Asp Ile Leu
165 170 175

Arg Ser Arg Asp Met Thr Thr Gly Ile Val Glu Asn Lys Phe Thr Phe
180 185 190

Lys Glu Leu Thr Phe Lys Met Val Asp Val Gly Gly Gln Arg Ser Glu
195 200 205

Arg Lys Lys Trp Ile His Cys Phe Glu Gly Val Thr Ala Ile Ile Phe
210 215 220

Cys Val Glu Leu Ser Gly Tyr Asp Leu Lys Leu Tyr Glu Asp Asn Gln
225 230 235 240

Thr Ser Arg Met Ala Glu Ser Leu Arg Leu Phe Asp Ser Ile Cys Asn
245 250 255

Asn Asn Trp Phe Ile Asn Thr Ser Leu Ile Leu Phe Leu Asn Lys Lys
260 265 270

Asp Leu Leu Ala Glu Lys Ile Arg Arg Ile Pro Leu Thr Ile Cys Phe
275 280 285

Pro Glu Tyr Lys Gly Gln Asn Thr Tyr Glu Glu Ala Ala Val Tyr Ile
290 295 300

Gln Arg Gln Phe Glu Asp Leu Asn Arg Asn Lys Glu Thr Lys Glu Ile
305 310 315 320

Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Ser Asn Ile Gln Phe Val
325 330 335

Phe Asp Ala Val Thr Asp Val Ile Ile Gln Asn Asn Leu Lys Tyr Ile
340 345 350

Gly Leu Cys
355

<210> 4
<211> 374
<212> PRT
<213> Artificial

<220>
<223> Synthetic

<300>

<301> SEJAL M. MODY, MAURICE K. C. HO, SUSHMA A. JOSHI, and YUNG H.
WONG

<302> Incorporation of Galphaz-Specific Sequence at the Carboxyl
Terminus Increases the Promiscuity of Galphai6 toward Gi-Coupled
Receptors

<303> The American Society for Pharmacology and Experimental
Therapeutics

<304> 57

<306> 13-23

<307> 2000

<400> 4

Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu
1 5 10 15

Asp Glu Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu
20 25 30

Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu
35 40 45

Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
50 55 60

Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro
65 70 75 80

Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala
85 90 95

Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His
100 105 110

Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu
115 120 125

Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile
130 135 140

Arg Ala Cys Tyr Glu Arg Arg Glu Phe His Leu Leu Asp Ser Ala
145 150 155 160

Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val

165

170

175

Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
180 185 190

Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp
195 200 205

Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu
210 215 220

Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
225 230 235 240

Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala
245 250 255

Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
260 265 270

Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr
275 280 285

Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp
290 295 300

Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr
305 310 315 320

Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Asn Arg Asn Lys Glu Thr
325 330 335

Lys Glu Ile Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Ser Asn Ile
340 345 350

Gln Phe Val Phe Asp Ala Val Thr Asp Val Ile Ile Gln Asn Asn Leu
355 360 365

Lys Tyr Ile Gly Leu Cys
370

<210> 5
<211> 858
<212> PRT

<213> Mus musculus

<400> 5

Met Pro Ala Leu Ala Ile Met Gly Leu Ser Leu Ala Ala Phe Leu Glu
1 5 10 15

Leu Gly Met Gly Ala Ser Leu Cys Leu Ser Gln Gln Phe Lys Ala Gln
20 25 30

Gly Asp Tyr Ile Leu Gly Leu Phe Pro Leu Gly Ser Thr Glu Glu
35 40 45

Ala Thr Leu Asn Gln Arg Thr Gln Pro Asn Ser Ile Pro Cys Asn Arg
50 55 60

Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val
65 70 75 80

Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly
85 90 95

Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Ser
100 105 110

Ser Leu Met Phe Leu Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr
115 120 125

Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
130 135 140

His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe
145 150 155 160

Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp
165 170 175

Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
180 185 190

Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp
195 200 205

Val Ala Ala Leu Gly Ser Asp Asp Asp Tyr Gly Arg Glu Gly Leu Ser
210 215 220

Ile Phe Ser Ser Leu Ala Asn Ala Arg Gly Ile Cys Ile Ala His Glu
225 230 235 240

Gly Leu Val Pro Gln His Asp Thr Ser Gly Gln Gln Leu Gly Lys Val
245 250 255

Leu Asp Val Leu Arg Gln Val Asn Gln Ser Lys Val Gln Val Val Val
260 265 270

Leu Phe Ala Ser Ala Arg Ala Val Tyr Ser Leu Phe Ser Tyr Ser Ile
275 280 285

His His Gly Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ser Trp Leu
290 295 300

Thr Ser Asp Leu Val Met Thr Leu Pro Asn Ile Ala Arg Val Gly Thr
305 310 315 320

Val Leu Gly Phe Leu Gln Arg Gly Ala Leu Leu Pro Glu Phe Ser His
325 330 335

Tyr Val Glu Thr His Leu Ala Leu Ala Asp Pro Ala Phe Cys Ala
340 345 350

Ser Leu Asn Ala Glu Leu Asp Leu Glu Glu His Val Met Gly Gln Arg
355 360 365

Cys Pro Arg Cys Asp Asp Ile Met Leu Gln Asn Leu Ser Ser Gly Leu
370 375 380

Leu Gln Asn Leu Ser Ala Gly Gln Leu His His Gln Ile Phe Ala Thr
385 390 395 400

Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln
405 410 415

Cys Asn Val Ser His Cys His Val Ser Glu His Val Leu Pro Trp Gln
420 425 430

Leu Leu Glu Asn Met Tyr Asn Met Ser Phe His Ala Arg Asp Leu Thr
435 440 445

Leu Gln Phe Asp Ala Glu Gly Asn Val Asp Met Glu Tyr Asp Leu Lys
450 455 460

Met Trp Val Trp Gln Ser Pro Thr Pro Val Leu His Thr Val Gly Thr
465 470 475 480

Phe Asn Gly Thr Leu Gln Leu Gln Gln Ser Lys Met Tyr Trp Pro Gly
485 490 495

Asn Gln Val Pro Val Ser Gln Cys Ser Arg Gln Cys Lys Asp Gly Gln
500 505 510

Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp
515 520 525

Cys Lys Ala Gly Ser Tyr Arg Lys His Pro Asp Asp Phe Thr Cys Thr
530 535 540

Pro Cys Asn Gln Asp Gln Trp Ser Pro Glu Lys Ser Thr Ala Cys Leu
545 550 555 560

Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Val Val Leu Ser
565 570 575

Leu Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Ala Leu Ala Leu
580 585 590

Gly Leu Ser Val His His Trp Asp Ser Pro Leu Val Gln Ala Ser Gly
595 600 605

Gly Ser Gln Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu
610 615 620

Ser Val Leu Leu Phe Pro Gly Arg Pro Ser Ser Ala Ser Cys Leu Ala
625 630 635 640

Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu
645 650 655

Phe Leu Gln Ala Ala Glu Thr Phe Val Glu Ser Glu Leu Pro Leu Ser
660 665 670

Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Leu Trp Ala Trp Leu
675 680 685

Val Val Leu Leu Ala Thr Phe Val Glu Ala Ala Leu Cys Ala Trp Tyr
690 695 700

Leu Asn Ala Phe Pro Pro Glu Val Val Thr Asp Trp Ser Val Leu Pro
705 710 715 720

Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Ser Leu Gly
725 730 735

Leu Val His Ile Thr Asn Ala Met Leu Ala Phe Leu Cys Phe Leu Gly
740 745 750

Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly
755 760 765

Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val
770 775 780

Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met
785 790 795 800

Gly Ala Ile Leu Val Cys Ala Leu Gly Ile Leu Val Thr Phe His Leu
805 810 815

Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Lys Leu Asn Thr Gln Glu
820 825 830

Phe Phe Leu Gly Arg Asn Ala Lys Lys Ala Ala Asp Glu Asn Ser Gly
835 840 845

Gly Gly Glu Ala Ala Gln Gly His Asn Glu
850 855

<210> 6
<211> 1353
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> GENBANK Accession no. M80632

<220>
<221> CDS

<222> (43)..(1164)

<400> 6	caggccctgt gatgtcacct ggtggctgt gaagcgccca cc atg gcc cg	tcc	54
	Met Ala Arg Ser		
	1		
	ctg act tgg ggc tgc tgt ccc tgg tgc ctg aca gag gag gag aag act		102
Leu Thr Trp Gly Cys Cys Pro Trp Cys Leu Thr Glu Glu Glu Lys Thr			
5	10	15	20
	gcc gcc aga atc gac cag gag atc aac agg att ttg ttg gaa cag aaa		150
Ala Ala Arg Ile Asp Gln Glu Ile Asn Arg Ile Leu Leu Glu Gln Lys			
25	30	35	
	aaa caa gag cgc gag gaa ttg aaa ctc ctg ctg ttg ggg cct ggt gag		198
Lys Gln Glu Arg Glu Leu Lys Leu Leu Leu Gly Pro Gly Glu			
40	45	50	
	agc ggg aag agt acg ttc atc aag cag atg cgc atc att cac ggt gtg		246
Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly Val			
55	60	65	
	ggc tac tcg gag gag gac cgc aga gcc ttc cgg ctg ctc atc tac cag		294
Gly Tyr Ser Glu Glu Asp Arg Arg Ala Phe Arg Leu Leu Ile Tyr Gln			
70	75	80	
	aac atc ttc gtc tcc atg cag gcc atg ata gat gcg atg gac cgg ctg		342
Asn Ile Phe Val Ser Met Gln Ala Met Ile Asp Ala Met Asp Arg Leu			
85	90	95	100
	cag atc ccc ttc agc agg cct gac agc aag cag cac gcc agc cta gtg		390
Gln Ile Pro Phe Ser Arg Pro Asp Ser Lys Gln His Ala Ser Leu Val			
105	110	115	
	atg acc cag gac ccc tat aaa gtg agc aca ttc gag aag cca tat gca		438
Met Thr Gln Asp Pro Tyr Lys Val Ser Thr Phe Glu Lys Pro Tyr Ala			
120	125	130	
	gtg gcc atg cag tac ctg tgg cgg gac gcg ggc atc cgt gca tgc tac		486
Val Ala Met Gln Tyr Leu Trp Arg Asp Ala Gly Ile Arg Ala Cys Tyr			
135	140	145	
	gag cga agg cgt gaa ttc cac ctt ctg gac tcc gcg gtg tat tac ctg		534
Glu Arg Arg Glu Phe His Leu Leu Asp Ser Ala Val Tyr Tyr Leu			
150	155	160	
	tca cac ctg gag cgc ata tca gag gac agc tac atc ccc act gcg caa		582
Ser His Leu Glu Arg Ile Ser Glu Asp Ser Tyr Ile Pro Thr Ala Gln			
165	170	175	180
	gac gtg ctg cgc agt cgc atg ccc acc aca ggc atc aat gag tac tgc		630
Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile Asn Glu Tyr Cys			
185	190	195	
	ttc tcc gtg aag aaa acc aaa ctg cgc atc gtg gat gtt ggt ggc cag		678
Phe Ser Val Lys Lys Thr Lys Leu Arg Ile Val Asp Val Gly Gly Gln			
200	205	210	

agg tca gag cgt agg aaa tgg att cac tgt ttc gag aac gtg att gcc	726
Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu Asn Val Ile Ala	
215 220 225	
ctc atc tac ctg gcc tcc ctg agc gag tat gac cag tgc cta gag gag	774
Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln Cys Leu Glu Glu	
230 235 240	
aac gat cag gag aac cgc atg gag gag agt ctc gct ctg ttc agc acg	822
Asn Asp Gln Glu Asn Arg Met Glu Glu Ser Leu Ala Leu Phe Ser Thr	
245 250 255 260	
atc cta gag ctg ccc tgg ttc aag agc acc tcg gtc atc ctc ttc ctc	870
Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val Ile Leu Phe Leu	
265 270 275	
aac aag acg gac atc ctg gaa gat aag att cac acc tcc cac ctg gcc	918
Asn Lys Thr Asp Ile Leu Glu Asp Lys Ile His Thr Ser His Leu Ala	
280 285 290	
aca tac ttc ccc agc ttc cag gga ccc cg ^g cga gac gca gag gcc gcc	966
Thr Tyr Phe Pro Ser Phe Gln Gly Pro Arg Arg Asp Ala Glu Ala Ala	
295 300 305	
aag agc ttc atc ttg gac atg tat gcg cgc gtg tac gcg agc tgc gca	1014
Lys Ser Phe Ile Leu Asp Met Tyr Ala Arg Val Tyr Ala Ser Cys Ala	
310 315 320	
gag ccc cag gac ggt ggc agg aaa ggc tcc cgc gcg cgc cgc ttc ttc	1062
Glu Pro Gln Asp Gly Arg Lys Gly Ser Arg Ala Arg Arg Phe Phe	
325 330 335 340	
gca cac ttc acc tgt gcc acg gac acg caa agc gtc cgc agc gtg ttc	1110
Ala His Phe Thr Cys Ala Thr Asp Thr Gln Ser Val Arg Ser Val Phe	
345 350 355	
aag gac gtg cgg gac tcg gtg ctg gcc cgg tac ctg gac gag atc aac	1158
Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu Asp Glu Ile Asn	
360 365 370	
ctg ctg tgacgcggga cagggAACCC caagcgcgac gcgtcggtggc gaggacatac	1214
Leu Leu	
ctccccctgg tggccgcgcg tggaaactgca ggtccaggag ctgccaagtg gggaaGCCAG	1274
cccacaggag agagtccctgc ttctactggg ccccaagCCA gctcctgtaa ttattcctcg	1334
ccttctcttag tgTTggaaag	1353

<210> 7
 <211> 29
 <212> DNA
 <213> Artificial

<220>

tac tcg gag gag gag cgc aag ggc ttc cgg ccc ctg gtc tac cag aac Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro Leu Val Tyr Gln Asn 70 75 80 85	474
atc ttc gtg tcc atg cgg gcc atg atc gag gcc atg gag cgg ctg cag Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala Met Glu Arg Leu Gln 90 95 100	522
att cca ttc agc agg ccc gag agc aag cac cac gct agc ctg gtc atg Ile Pro Phe Ser Arg Pro Glu Ser Lys His His Ala Ser Leu Val Met 105 110 115	570
agc cag gac ccc tat aaa gtg acc acg ttt gag aag cgc tac gct gcg Ser Gln Asp Pro Tyr Lys Val Thr Phe Glu Lys Arg Tyr Ala Ala 120 125 130	618
gcc atg cag tgg ctg tgg agg gat gcc ggc atc cgg gcc tgc tat gag Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile Arg Ala Cys Tyr Glu 135 140 145	666
cgt cgg cgg gaa ttc cac ctg ctc gat tca gcc gtg tac tac ctg tcc Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala Val Tyr Tyr Leu Ser 150 155 160 165	714
cac ctg gag cgc atc acc gag gag ggc tac gtc ccc aca gct cag gac His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val Pro Thr Ala Gln Asp 170 175 180	762
gtg ctc cgc agc cgc atg ccc acc act ggc atc aac gag tac tgc ttc Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile Asn Glu Tyr Cys Phe 185 190 195	810
tcc gtg cag aaa acc aac ctg cgg atc gtg gac gtc ggg ggc cag aag Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp Val Gly Gly Gln Lys 200 205 210	858
tca gag cgt aag aaa tgg atc cat tgt ttc gag aac gtg atc gcc ctc Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu Asn Val Ile Ala Leu 215 220 225	906
atc tac ctg gcc tca ctg agt gaa tac gac cag tgc ctg gag gag aac Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln Cys Leu Glu Glu Asn 230 235 240 245	954
aac cag gag aac cgc atg aag gag agc ctc gca ttg ttt ggg act atc Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala Leu Phe Gly Thr Ile 250 255 260	1002
ctg gaa cta ccc tgg ttc aaa agc aca tcc gtc atc ctc ttt ctc aac Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val Ile Leu Phe Leu Asn 265 270 275	1050
aaa acc gac atc ctg gag gag aaa atc ccc acc tcc cac ctg gct acc Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr Ser His Leu Ala Thr 280 285 290	1098
tat ttc ccc agt ttc cag ggc cct aag cag gat gct gag gca gcc aag	1146

Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp Ala Glu Ala Ala Lys				
295	300	305		
agg ttc atc ctg gac atg tac acg agg atg tac acc ggg tgc gtg gac			1194	
Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr Thr Gly Cys Val Asp				
310	315	320	325	
ggc ccc gag ggc agc aag aag ggc gca cga tcc cga cgc ctt ttc agc			1242	
Gly Pro Glu Gly Ser Lys Lys Gly Ala Arg Ser Arg Arg Leu Phe Ser				
330	335	340		
cac tac aca tgt gcc aca gac aca cag aac atc cgc aag gtc ttc aag			1290	
His Tyr Thr Cys Ala Thr Asp Thr Gln Asn Ile Arg Lys Val Phe Lys				
345	350	355		
gac gtg cgg gac tcg gtg ctc gcc cgc tac ctg gac gag atc aac ctg			1338	
Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu Asp Glu Ile Asn Leu				
360	365	370		
ctg tgaccaggc cccacctggg gcaggcggca cggcggcgcg ggtggaggt			1391	
Leu				
gggagtggct gcagggaccc tagtgtcctg gtctatctct ccagcctcgg cccacacgca			1451	
agggagtccgg gggacggccc gctgctggcc gctctttct ctgcctctca ccaggacagc			1511	
cgcggcccgag ggtactcctg ccctgcttg actcagttc ctcctttga aagggaaagga			1571	
gcacaaacggc catttggat gccagggtgg atgaaaaggt gaagaaatca ggggatttag			1631	
acttgggtgg gtgggcatct ctcaggagcc ccatctccgg gcgtgtcacc tcctggcag			1691	
ggttctggga ccctctgtgg gtgacgcaca ccctggatg gggctagtag agccttcagg			1751	
cgccttcggg cgtggactct ggccactct agtggacagg agaaggaacg cttccagga			1811	
acctgtggac taggggtgca gggacttccc tttgcaagggt gtaacagacc gctggaaaac			1871	
actgtcactt tcagagctcg gtggctcaca gcgtgtcctg ccccggttg cggacgagag			1931	
aaatcgccgc ccacaagcat ccccatccc ttgcaggctg gggctgggc atgctgcata			1991	
ttaacctttt gtatttattc ctcacaccc tgcaggctc cgtgcggcgt gaaattaaag			2051	
atttcttag			2060	

<210> 10
 <211> 2679
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> GENBANK Accession no. NM_002073

<220>
 <221> CDS
 <222> (13)...(1077)

<400> 10
 gagaccagga cc atg gga tgt cgg caa agc tca gag gaa aaa gaa gca gcc 51
 Met Gly Cys Arg Gln Ser Ser Glu Glu Lys Glu Ala Ala
 1 5 10

cg 15
 cg 20
 gg 25

Arg Arg Ser Arg Arg Ile Asp Arg His Leu Arg Ser Glu Ser Gln Arg 99

15 20 25

caa 30
 cg 35
 gc 40
 g 45

Gln Arg Arg Glu Ile Lys Leu Leu Leu Gly Thr Ser Asn Ser Gly 147

30 35 40 45

aag 45
 agc 50
 acc 55
 atc 60

Lys Ser Thr Ile Val Lys Gln Met Lys Ile Ile His Ser Gly Gly Phe 195

45 50 55 60

aac 65
 ctg 70
 gag 75

Asn Leu Glu Ala Cys Lys Glu Tyr Lys Pro Leu Ile Ile Tyr Asn Ala 243

65 70 75

atc 80
 gac 85
 tcg 90

Ile Asp Ser Leu Thr Arg Ile Ile Arg Ala Leu Ala Leu Arg Ile 291

80 85 90

gac 95
 ttc 100
 cac 105

Asp Phe His Asn Pro Asp Arg Ala Tyr Asp Ala Val Gln Leu Phe Ala 339

95 100 105

ctg 110
 acg 115
 ggc 120

Leu Thr Gly Pro Ala Glu Ser Lys Gly Glu Ile Thr Pro Glu Leu Leu 387

110 115 120

. 125

ggt 130
 gtc 135
 atg 140

Gly Val Met Arg Arg Leu Trp Ala Asp Pro Gly Ala Gln Ala Cys Phe 435

130 135 140

agc 145
 cgc 150
 tcc 155

Ser Arg Ser Glu Tyr His Leu Glu Asp Asn Ala Ala Tyr Tyr Leu 483

145 150 155

aac 160
 gac 165
 ctg 170

Asn Asp Leu Glu Arg Ile Ala Ala Asp Tyr Ile Pro Thr Val Glu 531

160 165 170

gac 175
 atc 180
 ctg 185

Asp Ile Leu Arg Ser Arg Asp Met Thr Thr Gly Ile Val Glu Asn Lys 579

175 180 185

ttc 190
 acc 195
 ttc 200

Phe Thr Phe Lys Glu Leu Thr Phe Lys Met Val Asp Val Gly Gly Gln 627

190 195 200

agg 205

tca gag cgc aaa aag tgg atc cac tgc ttc gag ggc gtc aca gcc 675

205

Arg Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu Gly Val Thr Ala			
210	215	220	
atc atc ttc tgt gtg gag ctc agc ggc tac gac ctg aaa ctc tac gag		723	
Ile Ile Phe Cys Val Glu Leu Ser Gly Tyr Asp Leu Lys Leu Tyr Glu			
225	230	235	
gat aac cag aca agt cgg atg gca gag agc ttg cgc ctc ttt gac tcc		771	
Asp Asn Gln Thr Ser Arg Met Ala Glu Ser Leu Arg Leu Phe Asp Ser			
240	245	250	
atc tgc aac aac aac tgg ttc atc aac acc tca ctc atc ctc ttc ctg		819	
Ile Cys Asn Asn Asn Trp Phe Ile Asn Thr Ser Leu Ile Leu Phe Leu			
255	260	265	
aac aag aag gac ctg ctg gca gag aag atc cgc cgc atc ccg ctc acc		867	
Asn Lys Lys Asp Leu Leu Ala Glu Lys Ile Arg Arg Ile Pro Leu Thr			
270	275	280	285
atc tgc ttt ccc gag tac aag ggc cag aac acg tac gag gag gcc gct		915	
Ile Cys Phe Pro Glu Tyr Lys Gly Gln Asn Thr Tyr Glu Glu Ala Ala			
290	295	300	
gtc tac atc cag cgg cag ttt gaa gac ctg aac cgc aac aag gag acc		963	
Val Tyr Ile Gln Arg Gln Phe Glu Asp Leu Asn Arg Asn Lys Glu Thr			
305	310	315	
aag gag atc tac tcc cac ttc acc tgc gcc acc gac acc agt aac atc		1011	
Lys Glu Ile Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Ser Asn Ile			
320	325	330	
cag ttt gtc ttc gac gcg gtg aca gac gtc atc ata cag aac aat ctc		1059	
Gln Phe Val Phe Asp Ala Val Thr Asp Val Ile Ile Gln Asn Asn Leu			
335	340	345	
aag tac att ggc ctt tgc tgaggagctg ggcccggggc gcctgcctat		1107	
Lys Tyr Ile Gly Leu Cys			
350	355		
ggtaaaaccc acgggggtgtc atgccccaaac gcgtgctaga gaggccaaat ccagggcag		1167	
aaaacagggg gcctaaagaa tgtccccac cccttggcct ctgcctcctt ggccccacat		1227	
ttctgcaaac ataaatattt acggatagat tgcttaggtag atagacacac acacatgcac		1287	
acacacacat ctggagatgg caaaatcctc taaaatgtcg aggtcttttg aagacttgag		1347	
aagctgtcac aaggtcacta caagcccaac ctgccccttc actttgcctt cctgagttgg		1407	
cccaactcca cttgggggtc tgcattggat tgtagggat aggcaagcagg gctgaggcaa		1467	
ggtaggccaa ctgcacccct gtcacctgga ggagggccgg ctcgctgccc gagctctggc		1527	
ctagggacct tgccgctgac caagagggag gaccagtgca gggtctgtgc accttccctg		1587	
ctggcctgca cacagctgct cagcaccatt tcattctgga cctggacact taggagccgg		1647	
gtgacagcac taaccagacc tccagccact cacagctttt tttaaaaaac agcttcaaaa		1707	

tatgcagcaa aaaccaatac aacaaaacga gtggcacat ttatttcaaa ctaggccagc	1767
tgggattcca gctttcttc tactagtctg atgtttata aatcaaaacc tggtttcct	1827
tctctggcat tttttttgt tttttgtttt ttgggttttt tttttttttt ggccaaatct	1887
cgtggtgttt cgcagaaaaa aatccagaaa atttcaaatg cagttgagta ttcttttta	1947
aatgcagatt ttcaaaacat atttttttc aggtggctt ttttgtctt ggcttgctga	2007
gtgtaaaagt tgttatctgg acgatctgtc tctctgctcc aaagaaattt tggagtgagt	2067
ggcagtcctg cgccagcctc gccccacacg tgggtacat aagcctctgc agtgcctct	2127
tgttaatggc ggggtttct gctttgtttt tatttaagaa aataaacacg acatatttaa	2187
agaaggttct ttcacctggg agcaaatgaa caatagctaa gtgtcttggt atttaaagag	2247
taaattattt gtggcttgc tgagtgaagg aaggggagca aggggtggc cccctggc	2307
cagcatgccc cgcgcctgag actggctgga aatgctctga ctcctgtgaa ggcacagcca	2367
gcgttgcgc ctgagggagg ccctgctggg accctgatct gggccttcct gtcccaggc	2427
cataggccaa ctgcgttgaa aggacgttcg ccaagggccg tggtaaata cgaactgcgc	2487
catggagagg agaggcactg ccggagccct tgccagatct ccctccctct ctctgtgcag	2547
tagctgttg tccgaggtca gtgtgcggaa tcacagccaa ggacgtgaag agatgtacgg	2607
ggaaaagaga agctggggat tggatgaaag tcaaaggttt tctactttaa gaaaataaaaa	2667
taccctgaat gg	2679

<210> 11
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic

<400> 11
 cgaagcttg actgaggcca cgcaccat

29

<210> 12
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic

<400> 12
 ctccttgggg cgggtgctgc ctcggggc

29

<210> 13		
<211> 30		
<212> DNA		
<213> Artificial		
<220>		
<223> Synthetic		
<400> 13		
ggcccccagg gcagcaaccg aaacaaggag		30
<210> 14		
<211> 37		
<212> DNA		
<213> Artificial		
<220>		
<223> Synthetic		
<400> 14		
gcattacgat gcggccgcag ctcctcagca aaggcca		37
<210> 15		
<211> 1122		
<212> DNA		
<213> Artificial		
<220>		
<223> Synthetic		
<220>		
<221> CDS		
<222> (1)..(1122)		
<300>		
<301> SEJAL M. MODY, MAURICE K. C. HO, SUSHMA A. JOSHI, and YUNG H. WONG		
<302> Incorporation of Galphaz-Specific Sequence at the Carboxyl Terminus Increases the Promiscuity of Galphai6 toward Gi-Coupled Receptors		
<303> The American Society for Pharmacology and Experimental Therapeutics		
<304> 57		
<306> 13-23		
<307> 2000		
<400> 15		
atg gcc cgc tcg acc tgg cgc tgc tgc ccc tgg tgc ctg acg gag		48
Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu		
1 5 10 15		
gat gag aag gcc gcc cgg gtg gac cag gag atc aac agg atc ctc		96
Asp Glu Lys Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu		

20	25	30	
ttg gag cag aag aag cag gac cgc ggg gag ctg aag ctg ctg ctt ttg			144
Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu			
35	40	45	
ggc cca ggc gag agc ggg aag agc acc ttc atc aag cag atg cgg atc			192
Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile			
50	55	60	
atc cac ggc gcc ggc tac tcg gag gag cgc aag ggc ttc cgg ccc			240
Ile His Gly Ala Gly Tyr Ser Glu Glu Arg Lys Gly Phe Arg Pro			
65	70	75	80
ctg gtc tac cag aac atc ttc gtg tcc atg cgg gcc atg atc gag gcc			288
Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala			
85	90	95	
atg gag cgg ctg cag att cca ttc agc agg ccc gag agc aag cac cac			336
Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His			
100	105	110	
gct agc ctg gtc atg agc cag gac ccc tat aaa gtg acc acg ttt gag			384
Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu			
115	120	125	
aag cgc tac gct gcg gcc atg cag tgg ctg tgg agg gat gcc ggc atc			432
Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile			
130	135	140	
cgg gcc tgc tat gag cgt cgg cgg gaa ttc cac ctg ctc gat tca gcc			480
Arg Ala Cys Tyr Glu Arg Arg Glu Phe His Leu Leu Asp Ser Ala			
145	150	155	160
gtg tac tac ctg tcc cac ctg gag cgc atc acc gag gag ggc tac gtc			528
Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val			
165	170	175	
ccc aca gct cag gac gtg ctc cgc agc cgc atg ccc acc act ggc atc			576
Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile			
180	185	190	
aac gag tac tgc ttc tcc gtg cag aaa acc aac ctg cgg atc gtg gac			624
Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp			
195	200	205	
gtc ggg ggc cag aag tca gag cgt aag aaa tgg atc cat tgt ttc gag			672
Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu			
210	215	220	
aac gtg atc gcc ctc atc tac ctg gcc tca ctg agt gaa tac gac cag			720
Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln			
225	230	235	240
tgc ctg gag gag aac aac cag gag aac cgc atg aag gag agc ctc gca			768
Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala			
245	250	255	

ttg ttt ggg act atc ctg gaa cta ccc tgg ttc aaa agc aca tcc gtc	816
Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val	
260 265 270	
atc ctc ttt ctc aac aaa acc gac atc ctg gag gag aaa atc ccc acc	864
Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr	
275 280 285	
tcc cac ctg gct acc tat ttc ccc agt ttc cag ggc cct aag cag gat	912
Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp	
290 295 300	
gct gag gca gcc aag agg ttc atc ctg gac atg tac acg agg atg tac	960
Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr	
305 310 315 320	
acc ggg tgc gtg gac ggc ccc gag ggc agc aac cgc aac aag gag acc	1008
Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Asn Arg Asn Lys Glu Thr	
325 330 335	
aag gag atc tac tcc cac ttc acc tgc gcc acc gac acc agt aac atc	1056
Lys Glu Ile Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Ser Asn Ile	
340 345 350	
cag ttt gtc ttc gac gcg gtg aca gac gtc atc ata cag aac aat ctc	1104
Gln Phe Val Phe Asp Ala Val Thr Asp Val Ile Ile Gln Asn Asn Leu	
355 360 365	
aag tac att ggc ctt tgc	1122
Lys Tyr Ile Gly Leu Cys	
370	

<210> 16
<211> 2529
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<223> GENBANK Accession no. AY032622

<220>
<221> CDS
<222> (1)..(2526)

<400> 16	
atg ctt ttc tgg gca gct cac ctg ctg ctc agc ctg cag ctg gcc gtt	48
Met Leu Phe Trp Ala Ala His Leu Leu Leu Ser Leu Gln Leu Ala Val	
1 5 10 15	
gct tac tgc tgg gct ttc agc tgc caa agg aca gaa tcc tct cca ggt	96
Ala Tyr Cys Trp Ala Phe Ser Cys Gln Arg Thr Glu Ser Ser Pro Gly	
20 25 30	
ttc agc ctc cct ggg gac ttc ctc ctg gca ggc ctg ttc tcc ctc cat	144
Phe Ser Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His	

35	40	45	
gct gac tgt ctg cag gtg aga cac aga cct ctg gtg aca agt tgt gac Ala Asp Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp			192
50	55	60	
agg tct gac agc ttc aac ggc cat ggc tat cac ctc ttc caa gcc atg Arg Ser Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met			240
65	70	75	80
cggttc acc gtt gag gag ata aac aac tcc aca gct ctg ctt ccc aac Arg Phe Thr Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn			288
85	90	95	
atc acc ctg ggg tat gaa ctg tat gac gtg tgc tca gag tct tcc aat Ile Thr Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ser Asn			336
100	105	110	
gtc tat gcc acc ctg agg gtg ccc gcc cag caa ggg aca ggc cac cta Val Tyr Ala Thr Leu Arg Val Pro Ala Gln Gln Gly Thr Gly His Leu			384
115	120	125	
gag atg cag aga gat ctt cgc aac cac tcc tcc aag gtg gtg gca ctc Glu Met Gln Arg Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Leu			432
130	135	140	
att ggg cct gat aac act gac cac gct gtc acc act gct gcc ctg ctg Ile Gly Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu			480
145	150	155	160
agc cct ttt ctg atg ccc ctg gtc agc tat gag gcg agc agc gtg atc Ser Pro Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Ile			528
165	170	175	
ctc agt ggg aag cgc aag ttc ccg tcc ttc ttg cgc acc atc ccc agc Leu Ser Gly Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Ile Pro Ser			576
180	185	190	
gat aag tac cag gtg gaa gtc ata gtg cgg ctg ctg cag agc ttc ggc Asp Lys Tyr Gln Val Glu Val Ile Val Arg Leu Leu Gln Ser Phe Gly			624
195	200	205	
tgg gtc tgg atc tcg ctc gtt ggc agc tat ggt gac tac ggg cag ctg Trp Val Trp Ile Ser Leu Val Gly Ser Tyr Gly Asp Tyr Gly Gln Leu			672
210	215	220	
ggc gta cag gcg ctg gag gag ctg gcc act cca cgg ggc atc tgc gtc Gly Val Gln Ala Leu Glu Glu Leu Ala Thr Pro Arg Gly Ile Cys Val			720
225	230	235	240
gcc ttc aag gac gtg gtg cct ctc tcc gcc cag gcg ggt gac cca agg Ala Phe Lys Asp Val Val Pro Leu Ser Ala Gln Ala Gly Asp Pro Arg			768
245	250	255	
atg cag cgc atg atg ctg cgt ctg gct cga gcc agg acc acc gtg gtc Met Gln Arg Met Met Leu Arg Leu Ala Arg Ala Arg Thr Thr Val Val			816
260	265	270	

gtg gtc ttc tct aac cgg cac ctg gct gga gtg ttc ttc agg tct gtg Val Val Phe Ser Asn Arg His Leu Ala Gly Val Phe Phe Arg Ser Val 275 280 285	864
gtg ctg gcc aac ctg act ggc aaa gtg tgg atc gcc tcc gaa gac tgg Val Leu Ala Asn Leu Thr Gly Lys Val Trp Ile Ala Ser Glu Asp Trp 290 295 300	912
gcc atc tcc acg tac atc acc aat gtg ccc ggg atc cag ggc att ggg Ala Ile Ser Thr Tyr Ile Thr Asn Val Pro Gly Ile Gln Gly Ile Gly 305 310 315 320	960
acg gtg ctg ggg gtg gcc atc cag cag aga caa gtc cct ggc ctg aag Thr Val Leu Gly Val Ala Ile Gln Gln Arg Gln Val Pro Gly Leu Lys 325 330 335	1008
gag ttt gaa gag tcc tat gtc cag gca gtg atg ggt gct ccc aga act Glu Phe Glu Glu Ser Tyr Val Gln Ala Val Met Gly Ala Pro Arg Thr 340 345 350	1056
tgc cca gag ggg tcc tgg tgc ggc act aac cag ctg tgc agg gag tgt Cys Pro Glu Gly Ser Trp Cys Gly Thr Asn Gln Leu Cys Arg Glu Cys 355 360 365	1104
cac gct ttc acg aca tgg aac atg ccc gag ctt gga gcc ttc tcc atg His Ala Phe Thr Thr Trp Asn Met Pro Glu Leu Gly Ala Phe Ser Met 370 375 380	1152
agc gct gcc tac aat gtg tat gag gct gtg tat gct gtg gcc cac ggc Ser Ala Ala Tyr Asn Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly 385 390 395 400	1200
ctc cac cag ctc ctg gga tgt acc tct ggg acc tgt gcc aga ggc cca Leu His Gln Leu Leu Gly Cys Thr Ser Gly Thr Cys Ala Arg Gly Pro 405 410 415	1248
gtc tac ccc tgg cag ctt ctt cag cag atc tac aag gtg aat ttc ctt Val Tyr Pro Trp Gln Leu Leu Gln Gln Ile Tyr Lys Val Asn Phe Leu 420 425 430	1296
cta cat aag aag act gta gca ttc gat gac aag ggg gac cct cta ggt Leu His Lys Lys Thr Val Ala Phe Asp Asp Lys Gly Asp Pro Leu Gly 435 440 445	1344
tat tat gac atc atc gcc tgg gac tgg aat gga cct gaa tgg acc ttt Tyr Tyr Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe 450 455 460	1392
gag gtc att ggt tct gcc tca ctg tct cca gtt cat cta gac ata aat Glu Val Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn 465 470 475 480	1440
aag aca aaa atc cag tgg cac ggg aag aac aat cag gtg cct gtg tca Lys Thr Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser 485 490 495	1488
gtg tgt acc agg gac tgt ctc gaa ggg cac cac agg ttg gtc atg ggt Val Cys Thr Arg Asp Cys Leu Glu Gly His His Arg Leu Val Met Gly	1536

500	505	510	
tcc cac cac tgc ttc gag tgc atg ccc tgt gaa gct ggg aca ttt			1584
Ser His His Cys Cys Phe Glu Cys Met Pro Cys Glu Ala Gly Thr Phe			
515	520	525	
ctc aac acg agt gag ctt cac acc tgc cag cct tgt gga aca gaa gaa			1632
Leu Asn Thr Ser Glu Leu His Thr Cys Gln Pro Cys Gly Thr Glu Glu			
530	535	540	
tgg gcc cct gag ggg agc tca gcc tgc ttc tca cgc acc gtg gag ttc			1680
Trp Ala Pro Glu Gly Ser Ser Ala Cys Phe Ser Arg Thr Val Glu Phe			
545	550	555	560
ttg ggg tgg cat gaa ccc atc tct ttg gtg cta tta gca gct aac acg			1728
Leu Gly Trp His Glu Pro Ile Ser Leu Val Leu Leu Ala Ala Asn Thr			
565	570	575	
cta ttg ctg ctg ctg att ggg act gct ggc ctg ttt gcc tgg cgt			1776
Leu Leu Leu Leu Ile Gly Thr Ala Gly Leu Phe Ala Trp Arg			
580	585	590	
ctt cac acg cct gtt gtg agg tca gct ggg ggt agg ctg tgc ttc ctc			1824
Leu His Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu			
595	600	605	
atg ctg ggt tcc ttg gta gct ggg agt tgc agc ctc tac agc ttc ttc			1872
Met Leu Gly Ser Leu Val Ala Gly Ser Cys Ser Leu Tyr Ser Phe Phe			
610	615	620	
ggg aag ccc acg gtg ccc gcg tgc ttg ctg cgt cag ccc ctc ttt tct			1920
Gly Lys Pro Thr Val Pro Ala Cys Leu Leu Arg Gln Pro Leu Phe Ser			
625	630	635	640
ctc ggg ttt gcc att ttc ctc tcc tgt ctg aca atc cgc tcc ttc caa			1968
Leu Gly Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln			
645	650	655	
ctg gtc atc atc ttc aag ttt tct acc aag gta ccc aca ttc tac cac			2016
Leu Val Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His			
660	665	670	
act tgg gcc caa aac cat ggt gcc gga ata ttc gtc att gtc agc tcc			2064
Thr Trp Ala Gln Asn His Gly Ala Gly Ile Phe Val Ile Val Ser Ser			
675	680	685	
acg gtc cat ttg ttc ctc tgt ctc acg tgg ctt gca atg tgg acc cca			2112
Thr Val His Leu Phe Leu Cys Leu Thr Trp Leu Ala Met Trp Thr Pro			
690	695	700	
cgg ccc acc agg gag tac cag cgc ttc ccc cat ctg gtg att ctt gag			2160
Arg Pro Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu			
705	710	715	720
tgc aca gag gtc aac tct gtg ggc ttc ctg gtg gct ttc gca cac aac			2208
Cys Thr Glu Val Asn Ser Val Gly Phe Leu Val Ala Phe Ala His Asn			
725	730	735	

atc ctc ctc tcc atc agc acc ttt gtc tgc agc tac ctg ggt aag gaa Ile Leu Leu Ser Ile Ser Thr Phe Val Cys Ser Tyr Leu Gly Lys Glu 740 745 750	2256
ctg ccg gag aac tat aac gaa gcc aaa tgt gtc acc ttc agc ctg ctc Leu Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu 755 760 765	2304
ctc cac ttc gta tcc tgg atc gct ttc acc atg tcc agc att tac Leu His Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ser Ser Ile Tyr 770 775 780	2352
cag ggc agc tac cta ccc gcg gtc aat gtg ctg gca ggg ctg gcc act Gln Gly Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Ala Thr 785 790 795 800	2400
ctg agt ggc ggc ttc agc ggc tat ttc ctc cct aaa tgc tac gtg att Leu Ser Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile 805 810 815	2448
ctc tgc cgt cca gaa ctc aac aac aca gaa cac ttt cag gcc tcc atc Leu Cys Arg Pro Glu Leu Asn Asn Thr Glu His Phe Gln Ala Ser Ile 820 825 830	2496
cag gac tac acg agg cgc tgc ggc act acc tga Gln Asp Tyr Thr Arg Arg Cys Gly Thr Thr 835 840	2529
<p><210> 17 <211> 2532 <212> DNA / <213> Mus musculus</p> <p><220> <221> misc_feature <223> GENBANK Accession No. AY032623</p> <p><220> <221> CDS <222> (1)..(2529)</p> <p><400> 17</p>	
atg gga ccc cag gcg agg aca ctc cat ttg ctg ttt ctc ctg ctg cat Met Gly Pro Gln Ala Arg Thr Leu His Leu Leu Phe Leu Leu His 1 5 10 15	48
gct ctg cct aag cca gtc atg ctg gta ggg aac tcc gac ttt cac ctg Ala Leu Pro Lys Pro Val Met Leu Val Gly Asn Ser Asp Phe His Leu 20 25 30	96
gct ggg gac tac ctc ctg ggt ggc ctc ttt acc ctc cat gcc aac gtg Ala Gly Asp Tyr Leu Leu Gly Gly Leu Phe Thr Leu His Ala Asn Val 35 40 45	144
aag agt gtc tct cac ctc agc tac ctg cag gtg ccc aag tgc aat gag Lys Ser Val Ser His Leu Ser Tyr Leu Gln Val Pro Lys Cys Asn Glu	192

50	55	60	
tac aac atg aag gtg ttg ggc tac aac ctc atg cag gcc atg cga ttc Tyr Asn Met Lys Val Leu Gly Tyr Asn Leu Met Gln Ala Met Arg Phe			240
65 70 75 80			
gcc gtg gag gaa atc aac aac tgt agc tct ttg ctg ccc ggc gtg ctg Ala Val Glu Glu Ile Asn Asn Cys Ser Ser Leu Leu Pro Gly Val Leu			288
85 90 95			
ctc ggc tac gag atg gtg gat gtc tgc tac ctc tcc aac aat atc cag Leu Gly Tyr Glu Met Val Asp Val Cys Tyr Leu Ser Asn Asn Ile Gln			336
100 105 110			
cct ggg ctc tac ttc ctg tca cag ata gat gac ttc ctg ccc atc ctc Pro Gly Leu Tyr Phe Leu Ser Gln Ile Asp Asp Phe Leu Pro Ile Leu			384
115 120 125			
aaa gac tac agc cag tac agg ccc caa gtg gtg gct gtt att ggc cca Lys Asp Tyr Ser Gln Tyr Arg Pro Gln Val Val Ala Val Ile Gly Pro			432
130 135 140			
gac aac tct gag tct gcc atc acc gtg tcc aac att ctc tcc tac ttc Asp Asn Ser Glu Ser Ala Ile Thr Val Ser Asn Ile Leu Ser Tyr Phe			480
145 150 155 160			
ctc gtg cca cag gtc aca tat agc gcc atc acc gac aag ctg caa gac Leu Val Pro Gln Val Thr Tyr Ser Ala Ile Thr Asp Lys Leu Gln Asp			528
165 170 175			
aag cgg cgc ttc cct gcc atg ctg cgc act gtg ccc agc gcc acc cac Lys Arg Arg Phe Pro Ala Met Leu Arg Thr Val Pro Ser Ala Thr His			576
180 185 190			
cac atc gag gcc atg gtg caa ctg atg gtt cac ttc cag tgg aac tgg His Ile Glu Ala Met Val Gln Leu Met Val His Phe Gln Trp Asn Trp			624
195 200 205			
atc gtg gtg ctg gtg agc gat gac gat tat ggc cga gag aac agc cac Ile Val Val Leu Val Ser Asp Asp Asp Tyr Gly Arg Glu Asn Ser His			672
210 215 220			
ctg ctg agc cag cgt ctg acc aac act ggc gac atc tgc att gcc ttc Leu Leu Ser Gln Arg Leu Thr Asn Thr Gly Asp Ile Cys Ile Ala Phe			720
225 230 235 240			
cag gag gtt ctg ccc gta cca gaa ccc aac cag gct gtg agg cct gag Gln Glu Val Leu Pro Val Pro Glu Pro Asn Gln Ala Val Arg Pro Glu			768
245 250 255			
gag cag gac caa ctg gac aac atc ctg gac aag ctg cgg cgg act tcg Glu Gln Asp Gln Leu Asp Asn Ile Leu Asp Lys Leu Arg Arg Thr Ser			816
260 265 270			
gcg cgt gtg gtg ata ttc tcg ccg gag ctg agc ctg cac aac ttc Ala Arg Val Val Val Ile Phe Ser Pro Glu Leu Ser Leu His Asn Phe			864
275 280 285			

ttc cgt gag gtg ctg cgc tgg aac ttc acg ggc ttt gtg tgg att gcc Phe Arg Glu Val Leu Arg Trp Asn Phe Thr Gly Phe Val Trp Ile Ala 290 295 300	912
tct gag tcc tgg gcc atc gac cct gtt cta cac aac ctc aca gag ctg Ser Glu Ser Trp Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu 305 310 315 320	960
cgc cac acg ggc act ttc ctg ggt gtc acc atc cag agg gtg tcc atc Arg His Thr Gly Thr Phe Leu Gly Val Thr Ile Gln Arg Val Ser Ile 325 330 335	1008
cct ggc ttc agc cag ttc cga gtg cgc cat gac aag cca ggg tat cgc Pro Gly Phe Ser Gln Phe Arg Val Arg His Asp Lys Pro Gly Tyr Arg 340 345 350	1056
atg cct aac gag acc agc ctg cgg act acc tgt aac cag gac tgc gac Met Pro Asn Glu Thr Ser Leu Arg Thr Thr Cys Asn Gln Asp Cys Asp 355 360 365	1104
gcc tgc atg aac atc act gag tcc ttc aac aac gtt ctc atg ctt tcg Ala Cys Met Asn Ile Thr Glu Ser Phe Asn Asn Val Leu Met Leu Ser 370 375 380	1152
ggg gag cgt gtg gtc tac agc gtg tac tcg gcc gtc tac gcg gtg gcc Gly Glu Arg Val Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala 385 390 395 400	1200
cac acc ctc cac aga ctc ctc cac tgc aat cag gtc cgc tgc acc aag His Thr Leu His Arg Leu Leu His Cys Asn Gln Val Arg Cys Thr Lys 405 410 415	1248
caa atc gtc tat cca tgg cag cta ctc agg gag atc tgg cat gtc aac Gln Ile Val Tyr Pro Trp Gln Leu Leu Arg Glu Ile Trp His Val Asn 420 425 430	1296
ttc acg ctc ctg ggc aac cag ctc ttc gac gaa caa ggg gac atg Phe Thr Leu Leu Gly Asn Gln Leu Phe Phe Asp Glu Gln Gly Asp Met 435 440 445	1344
ccg atg ctc ctg gac atc atc cag tgg cag tgg ggc ctg agc cag aac Pro Met Leu Leu Asp Ile Ile Gln Trp Gln Trp Gly Leu Ser Gln Asn 450 455 460	1392
ccc ttc caa agc atc gcc tcc tac tcc ccc acc gag acg agg ctg acc Pro Phe Gln Ser Ile Ala Ser Tyr Ser Pro Thr Glu Thr Arg Leu Thr 465 470 475 480	1440
tac att agc aat gtg tcc tgg tac acc ccc aac aac acg gtc ccc ata Tyr Ile Ser Asn Val Ser Trp Tyr Thr Pro Asn Asn Thr Val Pro Ile 485 490 495	1488
tcc atg tgt tct aag agt tgc cag cct ggg caa atg aaa aaa ccc ata Ser Met Cys Ser Lys Ser Cys Gln Pro Gly Gln Met Lys Lys Pro Ile 500 505 510	1536
ggc ctc cac cca tgc tgc ttc gag tgt gtg gac tgt ccg ccg gac acc Gly Leu His Pro Cys Cys Phe Glu Cys Val Asp Cys Pro Pro Asp Thr	1584

515	520	525	
tac ctc aac cga tca gta gat gag ttt aac tgt ctg tcc tgc ccg ggt Tyr Leu Asn Arg Ser Val Asp Glu Phe Asn Cys Leu Ser Cys Pro Gly 530	535	540	1632
tcc atg tgg tct tac aag aac aac atc gct tgc ttc aag cgg ccg ctg Ser Met Trp Ser Tyr Lys Asn Asn Ile Ala Cys Phe Lys Arg Arg Leu 545	550	555	1680
gcc ttc ctg gag tgg cac gaa gtg ccc act atc gtg gtg acc atc ctg Ala Phe Leu Glu Trp His Glu Val Pro Thr Ile Val Val Thr Ile Leu 565	570	575	1728
gcc gcc ctg ggc ttc atc agt acg ctg gcc att ctg ctc atc ttc tgg Ala Ala Leu Gly Phe Ile Ser Thr Leu Ala Ile Leu Leu Ile Phe Trp 580	585	590	1776
aga cat ttc cag acg ccc atg gtg cgc tcg gcg ggc ccc atg tgc Arg His Phe Gln Thr Pro Met Val Arg Ser Ala Gly Gly Pro Met Cys 595	600	605	1824
ttc ctg atg ctg gtg ccc ctg ctg gcg ttc ggg atg gtc ccc gtg Phe Leu Met Leu Val Pro Leu Leu Ala Phe Gly Met Val Pro Val 610	615	620	1872
tat gtg ggc ccc ccc acg gtc ttc tcc tgt ttc tgc cgc cag gct ttc Tyr Val Gly Pro Pro Thr Val Phe Ser Cys Phe Cys Arg Gln Ala Phe 625	630	635	1920
ttc acc gtt tgc ttc tcc gtc tgc ctc tcc tgc atc acg gtg cgc tcc Phe Thr Val Cys Phe Ser Val Cys Leu Ser Cys Ile Thr Val Arg Ser 645	650	655	1968
ttc cag att gtg tgc gtc ttc aag atg gcc aga cgc ctg cca agc gcc Phe Gln Ile Val Cys Val Phe Lys Met Ala Arg Arg Leu Pro Ser Ala 660	665	670	2016
tac ggt ttc tgg atg cgt tac cac ggg ccc tac gtc ttc gtg gcc ttc Tyr Gly Phe Trp Met Arg Tyr His Gly Pro Tyr Val Phe Val Ala Phe 675	680	685	2064
atc acg gcc gtc aag gtg gcc ctg gtg gcg ggc aac atg ctg gcc acc Ile Thr Ala Val Lys Val Ala Leu Val Ala Gly Asn Met Leu Ala Thr 690	695	700	2112
acc atc aac ccc att ggc cgg acc gac ccc gat gac ccc aat atc ata Thr Ile Asn Pro Ile Gly Arg Thr Asp Pro Asp Asp Pro Asn Ile Ile 705	710	715	2160
atc ctc tcc tgc cac cct aac tac cgc aac ggg cta ctc ttc aac acc Ile Leu Ser Cys His Pro Asn Tyr Arg Asn Gly Leu Leu Phe Asn Thr 725	730	735	2208
agc atg gac ttg ctg ctg tcc gtg ctg ggt ttc agc ttc gcg tac gtg Ser Met Asp Leu Leu Leu Ser Val Leu Gly Phe Ser Phe Ala Tyr Val 740	745	750	2256

ggc aag gaa ctg ccc acc aac tac aac gaa gcc aag ttc atc acc ctc	2304
Gly Lys Glu Leu Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu	
755 760 765	
agc atg acc ttc tcc acc tcc tcc atc tcc ctc tgc acg ttc atg	2352
Ser Met Thr Phe Ser Phe Thr Ser Ser Ile Ser Leu Cys Thr Phe Met	
770 775 780	
tct gtc cac gat ggc gtg gtc acc atc atg gat ctc ctg gtc act	2400
Ser Val His Asp Gly Val Leu Val Thr Ile Met Asp Leu Leu Val Thr	
785 790 795 800	
gtg ctc aac ttt ctg gcc atc ggc ttg ggg tac ttt ggc ccc aaa tgt	2448
Val Leu Asn Phe Leu Ala Ile Gly Leu Gly Tyr Phe Gly Pro Lys Cys	
805 810 815	
tac atg atc ctt ttc tac ccg gag cgc aac act tca gct tat ttc aat	2496
Tyr Met Ile Leu Phe Tyr Pro Glu Arg Asn Thr Ser Ala Tyr Phe Asn	
820 825 830	
agc atg att cag ggc tac acg atg agg aag agc tag	2532
Ser Met Ile Gln Gly Tyr Thr Met Arg Lys Ser	
835 840	

<210> 18
 <211> 2577
 <212> DNA
 <213> Mus musculus

<220>		
<221> CDS		
<222> (1)..(2574)		
<400> 18		
atg cca gct ttg gct atc atg ggt ctc agc ctg gct gct ttc ctg gag	48	
Met Pro Ala Leu Ala Ile Met Gly Leu Ser Leu Ala Ala Phe Leu Glu		
1 5 10 15		
ctt ggg atg ggg gcc tct ttg tgt ctg tca cag caa ttc aag gca caa	96	
Leu Gly Met Gly Ala Ser Leu Cys Leu Ser Gln Gln Phe Lys Ala Gln		
20 25 30		
ggg gac tac ata ctg ggc ggg cta ttt ccc ctg ggc tca acc gag gag	144	
Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Ser Thr Glu Glu		
35 40 45		
gcc act ctc aac cag aga aca caa ccc aac agc atc ccg tgc aac agg	192	
Ala Thr Leu Asn Gln Arg Thr Gln Pro Asn Ser Ile Pro Cys Asn Arg		
50 55 60		
ttc tca ccc ctt ggt ttg ttc ctg gcc atg gct atg aag atg gct gtg	240	
Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val		
65 70 75 80		
gag gag atc aac aat gga tct gcc ttg ctc cct ggg ctg cgg ctg ggc	288	
Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly		

85	90	95	
tat gac cta ttt gac aca tgc tcc gag cca gtg gtc acc atg aaa tcc Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Ser 100	105	110	336
agt ctc atg ttc ctg gcc aag gtg ggc agt caa agc att gct gcc tac Ser Leu Met Phe Leu Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr 115	120	125	384
tgc aac tac aca cag tac caa ccc cgt gtg ctg gct gtc atc ggc ccc Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val ,Leu Ala Val Ile Gly Pro 130	135	140	432
cac tca tca gag ctt gcc ctc att aca ggc aag ttc ttc agc ttc ttc His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe 145	150	155	480
ctc atg cca cag gtc agc tat agt gcc agc atg gat cgg cta agt gac Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp 165	170	175	528
cgg gaa acg ttt cca tcc ttc ttc cgc aca gtg ccc agt gac cgg gtg Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val 180	185	190	576
cag ctg cag gca gtt gtg act ctg ttg cag aac ttc agc tgg aac tgg Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp 195	200	205	624
gtg gcc gcc tta ggg agt gat gat gac tat ggc cgg gaa ggt ctg agc Val Ala Ala Leu Gly Ser Asp Asp Asp Tyr Gly Arg Glu Gly Leu Ser 210	215	220	672
atc ttt tct agt ctg gcc aat gca cga ggt atc tgc atc gca cat gag Ile Phe Ser Ser Leu Ala Asn Ala Arg Gly Ile Cys Ile Ala His Glu 225	230	235	720
ggc ctg gtg cca caa cat gac act agt ggc caa cag ttg ggc aag gtg Gly Leu Val Pro Gln His Asp Thr Ser Gly Gln Gln Leu Gly Lys Val 245	250	255	768
ctg gat gta cta cgc caa gtg aac caa agt aaa gta caa gtg gtg gtg Leu Asp Val Leu Arg Gln Val Asn Gln Ser Lys Val Gln Val Val Val 260	265	270	816
ctg ttt gcc tct gcc cgt gct gtc tac tcc ctt ttt agt tac agc atc Leu Phe Ala Ser Ala Arg Ala Val Tyr Ser Leu Phe Ser Tyr Ser Ile 275	280	285	864
cat cat ggc ctc tca ccc aag gta tgg gtg gcc agt gag tct tgg ctg His His Gly Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ser Trp Leu 290	295	300	912
aca tct gac ctg gtc atg aca ctt ccc aat att gcc cgt gtg ggc act Thr Ser Asp Leu Val Met Thr Leu Pro Asn Ile Ala Arg Val Gly Thr 305	310	315	960

gtg ctt ggg ttt ttg cag cgg ggt gcc cta ctg cct gaa ttt tcc cat		1008
Val Leu Gly Phe Leu Gln Arg Gly Ala Leu Leu Pro Glu Phe Ser His		
325	330	335
tat gtg gag act cac ctt gcc ctg gcc gct gac cca gca ttc tgt gcc		1056
Tyr Val Glu Thr His Leu Ala Leu Ala Asp Pro Ala Phe Cys Ala		
340	345	350
tca ctg aat gcg gag ttg gat ctg gag gaa cat gtg atg ggg caa cgc		1104
Ser Leu Asn Ala Glu Leu Asp Leu Glu Glu His Val Met Gly Gln Arg		
355	360	365
tgt cca cgg tgt gac gac atc atg ctg cag aac cta tca tct ggg ctg		1152
Cys Pro Arg Cys Asp Asp Ile Met Leu Gln Asn Leu Ser Ser Gly Leu		
370	375	380
ttg cag aac cta tca gct ggg caa ttg cac cac caa ata ttt gca acc		1200
Leu Gln Asn Leu Ser Ala Gly Gln Leu His His Gln Ile Phe Ala Thr		
385	390	395
tat gca gct gtg tac agt gtg gct caa gcc ctt cac aac acc cta cag		1248
Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln		
405	410	415
tgc aat gtc tca cat tgc cac gta tca gaa cat gtt cta ccc tgg cag		1296
Cys Asn Val Ser His Cys His Val Ser Glu His Val Leu Pro Trp Gln		
420	425	430
ctc ctg gag aac atg tac aat atg agt ttc cat gct cga gac ttg aca		1344
Leu Leu Glu Asn Met Tyr Asn Met Ser Phe His Ala Arg Asp Leu Thr		
435	440	445
cta cag ttt gat gct gaa ggg aat gta gac atg gaa tat gac ctg aag		1392
Leu Gln Phe Asp Ala Glu Gly Asn Val Asp Met Glu Tyr Asp Leu Lys		
450	455	460
atg tgg gtg tgg cag agc cct aca cct gta tta cat act gtg ggc acc		1440
Met Trp Val Trp Gln Ser Pro Thr Pro Val Leu His Thr Val Gly Thr		
465	470	475
ttc aac ggc acc ctt cag ctg cag cag tct aaa atg tac tgg cca ggc		1488
Phe Asn Gly Thr Leu Gln Leu Gln Gln Ser Lys Met Tyr Trp Pro Gly		
485	490	495
aac cag gtg cca gtc tcc cag tgt tcc cgc cag tgc aaa gat ggc cag		1536
Asn Gln Val Pro Val Ser Gln Cys Ser Arg Gln Cys Lys Asp Gly Gln		
500	505	510
gtt cgc cga gta aag ggc ttt cat tcc tgc tgc tat gac tgc gtg gac		1584
Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp		
515	520	525
tgc aag gcg ggc agc tac cgg aag cat cca gat gac ttc acc tgt act		1632
Cys Lys Ala Gly Ser Tyr Arg Lys His Pro Asp Asp Phe Thr Cys Thr		
530	535	540
cca tgt aac cag gac cag tgg tcc cca gag aaa agc aca gcc tgc tta		1680
Pro Cys Asn Gln Asp Gln Trp Ser Pro Glu Lys Ser Thr Ala Cys Leu		

545	550	555	560	
cct cgc agg ccc aag ttt ctg gct tgg ggg gag cca gtt gtg ctg tca Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Val Val Leu Ser 565		570	575	1728
ctc ctc ctg ctg ctt tgc ctg gtg ggt cta gca ctg gct gct ctg Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Ala Leu Ala Ala Leu 580	585		590	1776
ggg ctc tct gtc cac cac tgg gac agc cct ctt gtc cag gcc tca ggt Gly Leu Ser Val His His Trp Asp Ser Pro Leu Val Gln Ala Ser Gly 595	600		605	1824
ggc tca cag ttc tgc ttt ggc ctg atc tgc cta ggc ctc ttc tgc ctc Gly Ser Gln Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu 610	615		620	1872
agt gtc ctt ctg ttc cca ggg cgg cca agc tct gcc agc tgc ctt gca Ser Val Leu Leu Phe Pro Gly Arg Pro Ser Ser Ala Ser Cys Leu Ala 625	630	635	640	1920
caa caa cca atg gct cac ctc cct ctc aca ggc tgc ctg agc aca ctc Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu 645		650	655	1968
ttc ctg caa gca gct gag acc ttt gtg gag tct gag ctg cca ctg agc Phe Leu Gln Ala Ala Glu Thr Phe Val Glu Ser Glu Leu Pro Leu Ser 660	665		670	2016
tgg gca aac tgg cta tgc agc tac ctt cgg gga ctc tgg gcc tgg cta Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Leu Trp Ala Trp Leu 675	680		685	2064
gtg gta ctg ttg gcc act ttt gtg gag gca gca cta tgt gcc tgg tat Val Val Leu Leu Ala Thr Phe Val Glu Ala Ala Leu Cys Ala Trp Tyr 690	695		700	2112
ttg aac gct ttc cca cca gag gtg gtg aca gac tgg tca gtg ctg ccc Leu Asn Ala Phe Pro Pro Glu Val Val Thr Asp Trp Ser Val Leu Pro 705	710	715	720	2160
aca gag gta ctg gag cac tgc cac gtg cgt tcc tgg gtc agc ctg ggc Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Ser Leu Gly 725		730	735	2208
ttg gtg cac atc acc aat gca atg tta gct ttc ctc tgc ttt ctg ggc Leu Val His Ile Thr Asn Ala Met Leu Ala Phe Leu Cys Phe Leu Gly 740	745		750	2256
act ttc ctg gta cag agc cag cct ggc cgc tac aac cgt gcc cgt ggt Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly 755	760		765	2304
ctc acc ttc gcc atg cta gct tat ttc atc acc tgg gtc tct ttt gtg Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val 770	775		780	2352

ccc ctc ctg gcc aat gtg cag gtg gcc tac cag cca gct gtg cag atg	2400
Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met	
785 790 795 800	
ggt gct atc cta gtc tgt gcc ctg ggc atc ctg gtc acc ttc cac ctg	2448
Gly Ala Ile Leu Val Cys Ala Leu Gly Ile Leu Val Thr Phe His Leu	
805 810 815	
ccc aag tgc tat gtg ctt ctt tgg ctg cca aag ctc aac acc cag gag	2496
Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Lys Leu Asn Thr Gln Glu	
820 825 830	
ttc ttc ctg gga agg aat gcc aag aaa gca gca gat gag aac aat ggc	2544
Phe Phe Leu Gly Arg Asn Ala Lys Lys Ala Ala Asp Glu Asn Ser Gly	
835 840 845	
ggt ggt gag gca gct cag gga cac aat gaa tga	2577
Gly Gly Glu Ala Ala Gln Gly His Asn Glu	
850 855	
<210> 19	
<211> 29	
<212> DNA	
<213> Artificial	
<220>	
<223> Synthetic	
<400> 19	
ggaattcatg ctttctggg cagtcacc	29
<210> 20	
<211> 38	
<212> DNA	
<213> Artificial	
<220>	
<223> Synthetic	
<400> 20	
gcattacgat gcggccgctc aggttagtgcc gcagcgcc	38
<210> 21	
<211> 27	
<212> DNA	
<213> Artificial	
<220>	
<223> Synthetic	
<400> 21	
ggaattcatg ggaccccaagg cgaggac	27
<210> 22	

<211> 40
<212> DNA
<213> Artificial

<220>
<223> Synthetic

<400> 22
gcattacgat gcggccgcct agctcttcct catcgtgttag 40

<210> 23
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Synthetic

<400> 23
ggaattcatg ccagctttgg ctatcatgg 29

<210> 24
<211> 41
<212> DNA
<213> Artificial

<220>
<223> Synthetic

<400> 24
gcattacgat gcggccgcct attcatttg ttcctgagct g 41